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MGHTRRQGISPSKCPYINFFQLLVLAGLSHFCSG--VIHVTKEVKSVATLSCGHNVSVBELAQTRIYRQKEKNMVLTMMS MGKTIMKWGSLPPKRPCLALSQLLVLTGLFYFCSGTTPKSVTKRVKETVMLSCDYNTSTBELTSLRIYWQKDSKAVLALLP MGHTERPGTPLPRCLHLKLCLLLALAGLHPSSG----ISQVTKSVKEMAALSCDYNISIDELARMRIYWQKDQQMVLSIIS MGHTLRPGTPLPRCLHLKLCLLLLALACLHFSSG----ISQVTKSVKEMAALSCDYNISIDELARMRIYMQKDQQMVLSIIS MGHIMKAGSLPPKRPCLALSQLLVLIGLFYFCSGITPKSVTKRVKETVALSCDYSISIBBLISLRIYWQKDSKAALLLP MGKTMXWGSLPPKRPCLMLSQLLVLTGLFYFCSG1TPKSVTKRVKETVMLSCDYSTSTRBLTSLR1YWQXDSKMVLA1LP MGHTIMKWGSLPPKRPCLWLSQLLVLTGLFYFCSGI TPKSVTKRVKETVMLSCDXSTSTEBLTSLRI YWQKDSKMVLAI LP MGHIMKMGSLPPKRPCLWLSQLLVLFGLFYFCSGITPKSVTKRVKETVMLSCDYNTSTEBLTSLRIYWQKDSKANLAILP mghtwkwgslppkrpclnlsqllvltglfypcsgitpksvtkrvketvmlscdyntstebltslriywqkdsraylailp MGHTMKWGSLPPKRPCLWLSQLLVLTGLFYFCSG1TPKSVTKRVKETVMLSCDYSTSTEBLTBLR1YWQXDSXMYLA1LP MGHTMKHOSLPPKRPCLHLSQLLVLTGLFYFCSG11PKSVTKRVKETVMLSCDYNTSTEBLTSLR1YWQXDSKAVLA1LP mohtmykerslppkrpclalsollvliglpypcsgitpksvikrvketvmlscdyntsterlislriyaqkdskanlailp mohtnyknosi.PPKR.PCI/nlsqlavi.tgleyfcsoi.tpksvtkrvketvmlscdyntsteri.fslriyngkdsknylai.LP MGHTWKWGSLPPKRPCLWLSQLLVLTGLPYPCSGITPKSVTKRVKETVMLSCDYNTSTEBLTGLRIYWQKDSKWVLAILP mghthnomrslppkrpccmlsqllvljglpypcsgltpksvtkrvketvmlscdyststerljslriymqkdskall MGHTMKWGSLPPKRPCLWLSQLLVLTGLPYPCSGITPKSVTKRVKETVMLSCDYNASTRELTSLRIYMQKDSKWVLAILP MGHTWKWGSLPPKRPCLWLSQLLVLTGLFYFCSGITPKSVTKRVKETVMLSCDYSTSTEELTGLRIYWGKGKWTAILP mghthkngslppkrpcialsqlivliglppppcsgltpksvtkrvketvalscdyststeeltslriyaqkdsilp MGHTLRPGTPLPRCLHLKLCLLLALAGLHFSSG---1SQVTKSVKEMAALSCDYNISIDELARMRIYMQXDQQMVLSIIS mghtinkngslippkrpclalsollvligleyfcsgi tpksvtkrvketvalscdyntsteelislriyaqxdskavlailp MGHTMKNGSLPPKRPCLMLSQLLVLTGLPYPCSGTTPKSVTKRVKETVMLSCDYNTSTEELTSLRIYNQKDSKWYLAILP mghtwkwgslppkrpclmlsqllvltglpypcsgltpksvtkrvkbtvnlscdyststrellterlywgkdskwylatlp MGHTMKWGSLPPKRPCL#LSQLLVLIGLRYRCSGITPKSVTKRVKBTVMLSCDYNTSTBELTSLRIYWRDSKMXLAILP MGHTWKWGSLPPKCPCLMLSQLLVLTGLPYPCSGITPKSVTKRVKETVMLSCDYNTSTBELTSLRIYNQKDSKAVLAILP MGHTMKWGSLPPKRPCLWISQLLVLTGLPYRCSGITPKSVTKRVKETVNLGCDYNTSTBKLTSLRIYMQKDSKMYLAILP MOHTMKWGSLPPKRPCLMLSQLLVLTGLRYPCSGITPKSVTKRVKBTVNLSCDYNTSTEELTSLRIYMQKDSKMVLAILP MGHTWKWGSLPPKRPCLHIPQLLVITGLPYPCSGITPKSVTKRVKETVMLSCDYNTSTBELJSERIYWQKOSKWNLAILP MGHTMKWGSLPPKRPCLMLSQLLVLTGLPYPCSGITPKSVTKRVKBTVMPSCDYSTSTBELTSLRIYMQKOSKMVLAILP NGHTWANGSLPPARPCLWISQLLVLTGLPYPCSGITPKSVTKRVKETVNLSCDYNTSTERLTSLRIYMQKDSKANLAILP MGHTWKWGSLPPKRPCLWLSQLLVLTGLPYPCSGITPKSVTKRVKRTVMLSCDYNTSTRELTSLRIYRQKDSKWVLAILP MGHTMINGSLIPPKRPCLMLSQLLVLTGLPYFCSG1TPKSVTKRVKBTVNLSCDYSTSTBELTSLR1YNQXDSIMVLA1LP mahtmknasippkrpcialsollvijiglrypcsgiipksvikrvkrtvalscdyntsteeljslriyaqkdbraylailp MCHTWKWGSLPPKRPCLWLSQLLVLAGLPY FCSGLTPKSVTKRVKBTVMLSCDYSTSTRELTSLR1YWQKDSRAVLALLP MGHTMKRGSLPPKRPCLMPSQLLVLTGLPY PCSGTTPKSVTKRVKBTVMLSCDYNTSTRELTSLR1YHQKOSKAVLATLP Extracellular domain (ECD) --Signal sequence 3 Ξ 3 Ξ Ξ Ξ 3 3 Ξ 33 Ξ 7 Ê Ξ 3 Ξ SEQ: 056_R2_C028BP-5 SEQ: 057_R2_C028BP-6 SEQ: 058_R2_C028BP-7 SEQ: 058_R2_C028BP-8 SEQ: 060_R2_C028BP-9 SEQ: 061_R2_C028BP-10 SEQ:062_R2_CD28BP-11 SEQ:063_R2_CD28BP-12 SEQ:064_R2_CD28BP-13 SEQ:065_R2_CD28BP-14 SEQ:066_R2_CD28BP-15 SEQ.1.75_cd28A4.9 SEQ.1.77_cd28A6.9 SEQ.1.79_cd28A6.1 SEQ.1.79_cd28A8-4 SEQ.1.80_cd28A8-6 SEQ.1.80_cd28A8-6 SEQ.1.81_cd28A8-8 SEQ.1.81_cd28A8-1 SEQ.1.81_cd28B4-3 SEQ: 050_R1_Clone_118 SEQ: 051_R1_Clone_126 SEQ: 054_R2_CD28BP-3 SEQ: 055_R2_CD28BP-4 SEQ:067_R2_CD28BP-16 SEQ:068_R2_CD28BP-17 SEQ:174_Cd28A12-5 SBQ: 278_Human_B7-1 SEQ:048_R1_Clone_71 SEQ:049_R1_Clone_84 SEQ: 052_R2_CD28BP-1 SEQ: 053_R2_CD28BP-2 SEQ: 175_cd28a4 - 58tar SBQ:184_cd28b6-6 SEQ:185 cd28b8-5star SEQ:186 cd28c11-5

Fig. 2A

MGHIMKNGSLPPKRPCLMLSQLLVLTGLFTFCSGIJPKSVTKRVKETVMLSCDYSTSTEELTSLRIYWQKDSKAVLAILP MGHTMRWGSLPPKRPCLMLSQLLVLTGLPYFCSGITPKSVTKRVKETVMLSCDYSTSTBELTSLRIYWOXOSKWYLAILP MGKTMKNGSLPPKRPCLMLSQLLVITGLPYPCSGITPKSVTKRVKETVMLSCDYNTSTBELTSLRIYWQKDSKMVLAILP MGHTMKWGSLPPKRPCLMLSQLLVLTGLFYFCSGTTPKSVTKRVKZTVMLSCDYSTSTBBLTSLRIYWQKDSKMJLAILP MGHTURPGTPLPRCLALKLCLLLALAGLKFSSG---1SQVTKSVKEMAALSCDYNISIDELARMRIYWQKDQQMVLSIIS MGHTMKWGSLPPKRPCLMLSQLLVITGLPYFCSGITPKSYTKRVKETVMLSCDYNTSTEELTSLRIYWQKDSXMVLAILP MGHTMKWGSLPPKRPCLNLSQLLVLKQLPYFCSGITPKSVTKRVKETVMLSCDYNTSTBELTSLRIYWQKDSKMVLAILP MOHTWKWGSI.PPKRPCLWI.SQLLVLIGI.PYFC3GITPKSVTKRVKETVMI.SCDYSTSTBBLTSI.RIYWQKDSKWVLAII.P mahtmkmasi.Ppkapolmi.sqi.ivi.tgi.Pvposgi.tpksvtkkvketvmi.sodyntsteri.tsi.riykdskonvi.ai.lp MONTHYKKGSLPPKRPCL#LSQLLVLTGLFYFCSGTTPKSVTKRVKETVMLSCDYSTSTERLTSLRIYNGKOSKAVLATLP MOHTMEMGSLPPKRPCLMLSQLLVLTGLFYFCSGTTPKSVTKRVKETVMLSCDYNTSTEELTSLRIYMQXDSKMVLAILP mahtmamgslpparpclmlsqllvltglfyfcsgttprsvtarvastvmlscdyststbeltslriymqrdsnyllallp mghtmkmgsldprkppclmlsqllvliglfyfcsgltpksvtkrvkbtvmlscoyststeeltslriymqxdskmvlaild mghtmkmgslepprrpclalsollivlitglfyfcsgitpksvitkrvkbtvalscdyntsteeltslriyadskavlaild MGHTWKWGSLPPKRPCL#LSQLLVL/GLFYFCSGITPKSVTKRVKBTVMLSCDYNTSTEBLFSLRIYWGXOSKWYLAILP mghtmkmgslppkrpclalsqllvlitglfpvpcsgttpksvtvkvkbtvalscdyntstbeltslriyndskavvlailp MGHTMKMGSL.PPKRPCLKLSQLLVLTGL.FY FCSGTTPKSVTXRVKGTVML3CDYSTSTEELTGLRIYNQXDSKMVLAIL.P mghtmkmgslppkrpclalsqllvlidlfyfcsgttpksvtrrvkbtvalscdyntstbeltslriyndrdskavlailp MONTHKKMGSLIPPKR PCLMLSQLLVLITGLFY FCSGITIPKSVTKRVKBTVMLSCDYSTSTBELTSLRIYNQKDSKMVLAILP mghthkwigslppkrpciwlsqllvliglfyfcsgitpksvtkrvketvmlscoyntsteeltslriyngxdsravlailp MOHTMKMGSLPPKRPCLMLSQLLVLTGLFYPCSGTTPKSVTKRVKBTVMLSCDYNTSTBELTSLRIYNQKDSKMVLALLP MGHIMKNGSLPPKRPCLMLSQLLVLTGLFYPCSGITPKSVTKRVKRTVMLSCDYSTSELTSLRIYWQKDSXMVLALLP nghtmkmgslpprrpcialsqlivyltglfypcsgltpksvtkrvkstvalscdyntstbbltslriywokdskavlailp MGHTMKMGSLPPKRPCLMLSQLLVLTGLFYFCSGTTPKSVTKRVKGTVMLSCDYSTSTBELJSLRIYNQROSKMVLALLP mghtniongslppkrpclalsqllvligleyrcsgitpksvtkrvketvalscdyntstbeltslrlyrqkdskallp mghtwkngslppkrpclalsqllvliglpyfcsglipksvikrvketvalscdyntsteeljslriymqkdskavlailp mghtmkngbløpkrpclalsqlivliglfypcsgiipksvikkyketvalsciftbeltislriyagndskavlallp mohtmangslpparapcialsqllvligleypcsgltpksytkryketvmlscopyntsteeltseriypgdsrmylaild mghtwkwgslppkrpctalsQllvvltglpypcsgttpksvtkrvketvmlscdyntsteeljtslr1y4qkdskavlaild mghtwkngslppkrpctalsqllvtiglpypcsgitpksvtkkvketvmlgcdyntstbbltstriygkdskavllle mghtinkingsi.PPFKR.PCTailsQliviltgi.Py.PCSgtt.PKSVTKRVKETVMi.SCDYNTSTBBi.T9lktiynqxdbkrvilaii.D mghtimkingslippkripctalsqlilvtitglipypcsgjitpksvytkrvketvmlscdyntsteblitslriyaqkdsknyllaild mahtimkingsi ppkr pcimi sqilvilitqi ey pcsgi t pksvtkr vetvmi. Scdyntster i tsir i ymqkdskavila i dp mchtmkwgglppkrpclnlgqllvltglfprypcggltpksvtkrvketvnlscdyntstelltslhiynckornyllld mghtmangslppaapclalsollvloglpypcsgitpksvtaavketvmlscoysteeltslaiyncadanylailp mghtmkwgslppkrpclalsqllvlfglpypcsgitpksvtkrvketvmlscdyntsterltslifwqkdskmylailp Extracellular domain (ECD) Signal sequence -3 Ξ 3 3 3 Ξ 3 Ξ Ξ Ξ 3 3 3 33 3 Ξ 3 £ 3 3 ਰ ਰ 3 Ξ Ξ Ξ Ξ Ξ SEQ:216_cd2838-6 SEQ:217_cd2889-6 SEQ:218_cd2883-1 SEQ:192_cd28D2-3 SEQ:196_cd28D12-5 SEQ:197_cd28E10-6 SEQ: 203_cd28G1-5 SBQ: 204_cd28G1-9 SBQ: 205_cd28H4-3 SEQ:187_cd28C6-1 SEQ:188 cd28C7-3 SBQ: 189_cd28C8-6 SBQ:190 cd28c9-5star SEQ:191_cd28C2-4 SEQ:193_cd28D2-9 SED:194_cd28D8-9 SEQ:195_cd28D11-1 SEQ:198_cd28F7-2 SEQ:199_cd28F8-4 SRQ: 200 cd28F10-2 SEQ: 201 cd28F12-5star SEQ: 202_cd28G2-8 SEQ: 206_cd28H11-3 SEQ:207_cd28H6-6 SEQ:208_cd28E2-4 SE0:209_cd28B4-5a SEQ:210_cd28A2-5a SRQ:211 cd2884-58tar SEQ: 212_cd28D5-6 SEQ: 213_cd28D10-4 SEQ: 214_cd28E2-58tar SEQ: 215_cd28B5-2 SEQ: 219_cd28F3-5 SEQ: 221 cd28F11-8 980:283_CD28BP_Con SBQ:220 cd28F3-6

Fig. 2B

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	٠	Extracellular domain (ECD)
SEQ:278_Human_B7-1	(79)	81 GDMNI WPEYKNRT LFDI TINNISIVI LALRPSDEGTYECVVLK-YEKDAFKREHLARVTLSVKADFPTPSISDPEI PTSNI
SBQ: 048_R1_Clone_71	(81)	GKVQVWPBYKNRTITDAMDNPRIVILALRLSDSGTYTCVIOKPVLKGAYKLEHLASVRLMIRADFPVPTINDLGNPSPNI
SEQ:050 R1 Clone 118	(38)	GOVEWWPETKNRTFPDIINNLSLANILALRISDKGTYTCVVOK-NENGSFRREHLTSVTLSIRADSPVPSITDIGHPAPNV GOVEWPEXKNRTFPDIINNLSLANILALALPISLSDKGTYTCVVOK-NENGSPBERFREMTSSTESTRANDSPPSITDIGHPAPNV
SBO:051_R1_Clone_126	(81)	GKVQVIPBYKINFITTDMINDNERIVITALIZISDSGTYTCVIOKEDLKGAYKI. HIJ TSVRIMITADIZEVETINI CHEREKINI.
SEQ: 052_R2_CD28BP-1	(81)	GKVQVWPBYKNRTITOMNONERIVILALRISDSGTYTCVIQKPVLKGRYKLERILASVRLMIRADFPVFTINDLANPSPNI
SEQ: 053_R2_CD28BP-2	(81)	GKVQVWPBYKNRTITDMNDNPRIVILALRLSDSGTYTCVIQKPVLKGAYKLEHLASVRLMIRADFPVPTINDLGNPSPNI
SBQ: 055 R2 CD28BP-3	(81)	GKVQVMPEVKORTITDANDOPRIVILALRISDSGTYICVIQKPVLKGAYKLEHIASVRLMIRADPPVPTINDLGNPSPNI GKVOKAPEYXNRITIDANDNDRIVII.AI DI SARGOTATATIONERI VORVOT TITTA SARGOTATIONERI
SRQ: 056_R2_CD28BP-5	(81)	GXVQVNPEYKYRTITDMADDNERIVILALALALSDSGG IICV LEGA FARGA FALLALAGAS VILMI KADI FV FILMDLGANFENI GXVQVNPEYKYRTITDMADDNERIVILALALSDSKGTYTCVVDKPVLKGA VXI.SHT.SSVBI MTBADREVBETUNI GANFENI
SBQ: 057_R2_CD28BP-6	(81)	GXVQVWPEXXXRTITDMIDNPRIVILALRLSDSGTYTCVJOKPVLKGAYKKENIASVPI MIPBADPSVPITTITIO CONT
SEQ: 058_R2_CD28BP-7	(81)	GKVQVWPEXXNRTITDMIDNPRIVILALRISDSGTYTCVIQKGYLKGAYXZEHIASVRIMIRADPPUPTIKNITANDSDWIT
SEQ: 059_R2_CD28BP-8	(81)	GKVQVWPEXXNRTITDMIDNPRIVILALRISDSGTYTCVI QKPVLKGAYKLEHLASVRLMIRADFPVFSITOIGHPANNU
SBQ: 060_R2_CD28BP-9	(81)	GKVQVWPBYKXNTIIDMIDNIPRIVILALRLSDSGTYTCVIQKPVLKGAYKLEKLASVRLMIRADPPVPTINDIGANDSPNI
SEQ:061_R2_CD28BP-10	(81)	GKVQVWPRYXNRTITDANDNPRIVILALRLSDSGTYTCVIOKPVLKGAYKLEHLTSVRLMIRADPPVPTINDLGNPSPNI
SEQ:062_R2_CD28BP-11	(81)	GKVQVWPBYXNRTITDMNDNPRIVILALRLSDKGTYTCVVQK-NENGSPRREHLTBVTLSIRADFEVPSITDIGHPARMV
SEQ: 063_R2_CD28BP-12	(81)	GKVQVWPEYKNRTITDMONPRIVILALRLSDSGTYTCYIQKPVLXQAYKLBHLASVRLMIRADFPVPTINDLGNPSPWI
SBO: 064 R2 CD28BP-13	(81)	GKVQVWPEYNNRTITDMONDFIVILALALBUSDSGTYTCVIQKPVLXGAXKLEHLASVRLMIRADPPVPTINDLGNPSPNI
SEQ: 065 R2 CD28BP-14	(28)	GQVEVWPEYKNRTITDMMDNPRIVILALRLSDSGTTICVIQKPVLKGAYKLEHLASVRLMIRADFPVPTINDLGNSEDNI
SEQ:066_R2_CD28BP-15	(81)	GKVQVWPEYKNRTITDMYDNPRIVILALRPSDSGTYTCYIOKPVLKGAYKLEHLASVRLMIRADFPVPTINDLGNBSPNI
SEQ: 067 R2 CD288P-16	(81)	GKVQVWPEYKNRTITDMNDNPRIVILALRLSDSGTTTCVIQKDVLKGAYKLEHLTSVRLMIRADFPVPTINDLGNPSPNI
SEQ: 068 R2 CD2 8BP-17	(81)	GKVQVWPEYKNRTEPDIINNLSLMILALRLSDKGTTTCVVQK-NENGSFRREHLTSVTLSIRADFPVPSITDIGHPARN
SEQ: 174 cd28A12-5	(18)	GKVÖVMPEYKNRTITDMADNLRIVILALRLSDSGTTTCVIQKEDLKGAYKLRHLTSVRLMIRADEPVPTINDLGNESPNI
SECTION CONTRACTOR	(TR)	GKVQVWPBYXKTTTDMNDRPRIVILALRLSDSGTYTCVIQKPVLRGAYKLBHLTSVRLMIRADPPVPTINDLGNPSFNI
SEO: 177 CA2886-9	16	GNOVEWER INNET LIBERTONET IN LIBERTONET OF THE STATE OF T
SE0:178_cd28A6-1	(81)	GKVQVWPEYKARIITIDMNIDNPRIVILALBISDSGTTVPCVTORPVILKERBAKKERI AGIDI MIDADFPVPTINDLGNPGPNI GKVQVWPEYKARIITIDMNIDNPRIVILALBISDSGTVPCVTORPVILKEBVKI. BUI AGIDI MIDADSFNIMITATATA AGIDI MIDADSFNIMITATATA A
SEQ:179_cd28A8-4	(81)	GKVQVWPEXXXXIITDMXDNPRIVILALRISDSGTYTCVIOKPVILKONATISHITSYRLMIDBARDETISHI AARAA TAADAA AAAAA
SEQ:180_cd28A8-6	(81)	GKVQVWPEYNORTITDMXDNPRIVILALRISDSGTYTCVVOK · NENGSPRREHITSVTISTRANFOVPSTTTTI GUBB BAN
SEQ:181_cd26B2-8	(81)	GKVQV4PBYHQKTITDHGDDPRIVILALALSDKGTYTCVIQKPVLKGAYGEHLASVRLMIRADFPVFTINDIGNDSPWI
SBQ:182_cd28B4-3	(81)	GKVQVWPBYKNRTITDNNDNPRIVILALRLSDSGTYTCVIOKPVLKGAYKLEHLTSVRLMIRADFPUPTINDI, GNDSPNI
SEQ:183_cd28B6-3	(81)	GKVQVWPEYKNRTITDMXDNPRIVILALRLSDSGTYTCVIQKPDLKGAYKLEHL/TSVRLMIRADFPVPTINDLGNPSRVI
SEQ:184_cd28b6-6	(81)	GKVQVWPEYKNRTITDMXDNPRIVILALRLSDKGTYTCVIQKPVLKGAYKLEHLTSVTLSIRADPPVPSITDIGHPARNV
SE0:185_cd28b8-5star	(81)	GKVQVWPBYKNRTITJMNDNPRIVILALRLSDSGTYTCVIQKPVLKGAYKLEHLTSVRLMIBADPPVPTINDLGNBSPNI
SEQ:186_cd28c11-5	(81)	GKVQVWPBYKORTITDMONPRIV!LALRLSDSGTTTCVIQKPVLKGAYXLBHLTSVRLMIRADFPVPTINDLGNPSENI

Fig. 2C

GKVQVWPEYKNRTITDMNDNPRIVILALRLSDSGTYTCVIQKPDLKGAYKLBHLTSVRLMIRADFPVPSITDIGHPAPNV GKVQVWPEYRNRTITDMODNPRIVILALALSDSGTYTCVVQK-NRNGSFRREHLTSVTLSIRADFPVPSITDIGHPAPNV GKVQVWPEYKNRTITDANDNPRIVILALRLSDSGTYTCVIQKPVLKGAYKLEHLASVRLMIRADFPVPSITDIGHPAPNV GKVQVMPEYKRRTI TOMODNPRI VI LALALSDSGTYTCVI OKPOLKGAYKL BHLTSVRLMI RADFPVPSITDI CHPAPNV GKVQVMPEYKNRTITDANDNPRIVILALRLSDSGTYTCVIQKPDLKGAYKLEHLASVRLAIRAPPVPSITDIGHPAPNV GXVQVAPEYKRRTFPDI INNLSLMI LALRLSDXGTYTCVVQK-NRNGSFRRBHLTSVTLSI RADFPVSSITDIGHPAPNV GKVQVWPEYRNRTITDMDNPRIVILALRLSDSGTYTCVIQKPVLKGAYKLBHLTSVRLMIRADEPVPSITDIGHPAPNV GKVQVWPBYKNRTI TDMNDNPRI VI LALRLEDSGTYTCVI QKPDLKGAYKLBHLASVRLMI RADFPVPSI TDIGHPAPNV GKVQVWPRYGNRTITDMDNPRIVILALRLSDKGTTTCVVQKPDLKGAYALBHLASVPLMIRADFPVPSITDIGHPADNV GKVQVWPBYKNRTITDANDNPRIVILALRLSDKGTYTCVVQK-NENOSFRRHLTSVTLSIRADFPVPSITDIGHPAPNV GKVQVWPBYKNRTI TIDMNIDNPRIV I LALRLSDSGTYTCVVQK- NENGSFRREHLISVTLS I RADFPVPSITDI GHPAPNV gkvovmpryknrti tomnonpriv i lalrlsdsgtyt cviqkpvlkgayklehlt svrlmiradffyptindlgmpspni GKVQVWPBYKMRTITDMNDNPRIVILALRLSDSGTYTCVIQKPVLKGAYKLEHLASVRLMIRADPPVPTINDLGNPSPNI GKVQVWPEYKNRTITDMNDMPRIVILALRLSDSGTYTCVIQKPVIKGAYKLBHLASVRLMIRADFPVPTINDLGNPSPNI GOVEVWPEYKMRTITDANDNPRIVILALRLSDSGTYTCVIQKFVLKGAYKPEHLASVRLMIRADFPVPTINDLGNPSPNI GKVQVMPEYKORTI TDMGDDPRI VI QALRLSDSGTYTCVI QKPVLKGAYKLBHLASVRLMI RADFPVP - - TDLGNPSPNI GKVQVMPEYKMRTITDMVDNPRIVILALRLSDSGTYTCVIQKFVLKGAYKLEHLTSVRLMIRADFFVPTINDLGNPSPNI GKVQVMPEYKORTI IDMODNPRI VILALRLSDSGIYTCVI QKEVLKGAYKLEHLTSVRLMI RADFEVPTINDI GNPSPNI gkvovmpeyknrtitdmydnpriv ilalrledosgtytcviokpvlkcayklehlasvrlmiradfpyptindlknpspni GKVQVWPEYKGRTTTDAGDDVPRLVILALALSDSGTYTCVIQKPVLKGAYKLEHLASVRLAIRADFPVPTINDLGNPSPNI GKVQVMPBYKNRTITDMNDNPRIVILALRLSDSGTYTCVIQKPVLKGAYKLBHLASVRLMIRADFPVPTINDLGNPSPNI GKVQVWPEYKKRTITDANDNPRIVILALALSDSGTYTCVIQKEVLKGAYKLBHLASVRLMIRADFPVPSINDLGNPSDNI GKVQVWPEYKNRTITDMXDNPRIVILALRLSDSGFYTCVIQKPVLKGAVKLEHLASVRLMIRADFPVPTINDLGNPSBNI gkvqvmpzykorti tdamdnpri vi ialrlsdsgtttcvi qkpvlkkayklbhlasvrlmi radfpvptindlgnpsdn; GKVQV4PEYIGIRTI TDMADNPRIVIIALRESDSGTYTCVI QKPVLKGAYKLEHLASVRLMIRADFPVPTINDIGNPSPNI gkvovmpeyknrti tomdnpri vilalrlodkgtytcvi okpvlkgayklemlasvrlmi radffyptindi.Gnpsdni gkvovypryndri tdmiddpri vilalrledegtyttevi okpylkgayklehlasvrimi radfdyptindi. Gndspui gkvqvmpeyknrtitdmndnprivilalrlsdsgtytcviqkevlkgayklemlsvrlmiradppvptindlgnpspni gkvqvwpbymriitidmddpprivilalrpsdggtytcviqkpvlkgayklehlardrimiradfyvptindlgnpspni GXVQV#PBYRNRTITDM\DNPRIVILALRLSDSGTYTCVIQXPDLKGAYKLBHLASVRL#IRADFPVPTINDLGNPSPNI GKVQVWPRYKKRTI TOMNONPRI V I LALRLSDKGTYTCVI QKPDLKQAYKLEHLASVRLMI RADFPV PLI NOLGNPSPNI gkvqvmpbyknrti timndnpri v i lalrlsdsgtytcvi qkpdlkqayxlehli svrlmi radffvpti ndlgnpspni gkvovydeykntti tdmodder i vi lalelsdsgtytcvi okedlkgayklehli svrimi radfrvptindlgneseni GKVQVPPEXKNRTITDMODPRIVILALRLSDSGTYTCVIOKPVLKGAYKLEHLASVRLMIRADFPVPTINDLGNPSPNI gkvovppeyknrtitdandnprivilalrlsdsgtytcviokfylkgayklehlasvrlalradffvytindlgnpsdni GKVQVWPBYKMRTITDMNDNPRIVILALRLSDSGTYTCVIQKBYLKGAYKLRHLTSVRLAIRADFPVPTINDLGNPSPNI Extracellular domain (ECD) 81) (18) (18 (81) (81) (63) 8 (18) 9 61) 91 (81) 81 83 (81) 81) (81) 81) (81) (18) (83) 61 81) 81) (81) 81) 81) (18 (81) (81) (81) 81) SEQ: 203_cd28G1-5 SEQ: 204_cd28G1-9 SEQ: 205_cd28H4-3 SEQ: 206_cd28H11-3 SEQ:207_cd28H6-6 SEQ:208_cd28E2-4 SEQ:209_cd28E4-5a SEQ:210_cd28A2-5a SEQ: 216_cd28B8-6 SEQ: 217_cd28B9-6 SEQ: 218_cd28F3-1 SEQ: 219_cd28F3-5 SEQ: 220_cd28F3-6 SEQ:187_cd28C6-1 SEQ:188_cd28C7-3 SEQ:189_cd28C8-6 SEQ: 200_cd28F10-2 SEQ: 201_cd28F12-58tar SEQ:283_CD288P_Con SEQ: 190 cd28c9-5star SEQ:191_cd28C2-4 SEQ:192_cd28D2-3 SEQ:193_cd28D2-9 SEQ:194_cd28D8-9 SEQ: 196_cd28D12-5 SEQ: 197_cd28E10-6 SEQ:198_cd28F7-2 SEQ:199_cd28F8-4 SEQ: 202_cd28G2-8 SEQ:211_cd28B4-5star SEQ:212_cd28D5-6 SEQ: 213_cd28D10-4 SEQ:214 cd28B2-5star 3BQ:195_cd28D11-1 SEQ:215_cd28E5-2 cd28F11-8 SEO: 221

Fig. 2D

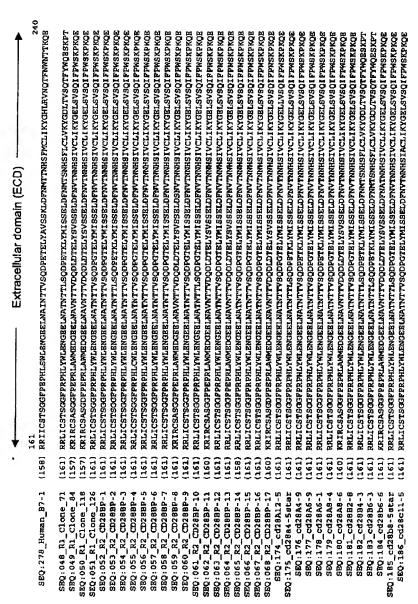


Fig. 2E

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Fig. 2F

COSSETT. CSCCI

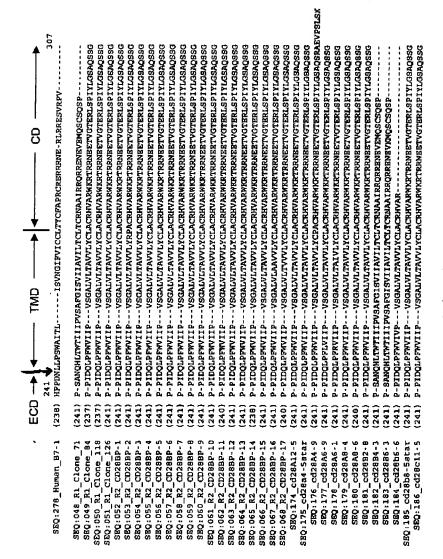


Fig. 2G

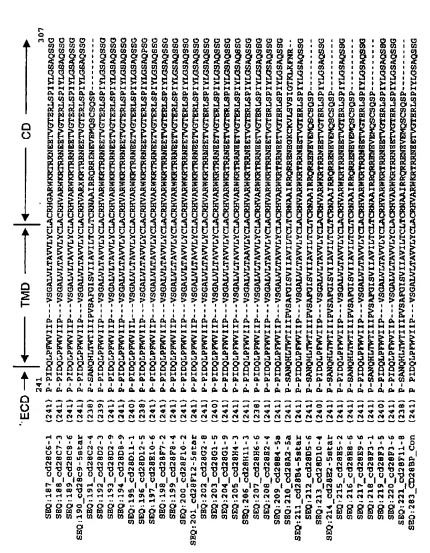


Fig. 2H

MGHTRRQGTSPSKCPYLNPFQLLVLAGLSHPCSQVIHVTXEVKEVATLSCGMIVSVEBLAQTRIYMQXBKKMVLTMMSGD Extracellular domain (ECD) Signal sequence

MSHTRRQGTSPSKCPYLK PPQLLIVILASILSHFCSGV I HNTKBVKEVATLSCGHNVSVEELAQTR I YRQKBKKNVLTRMSGD MGHTRRQGISPSKCPYLKPFQLLVVLAGLSHFCSGVIHVTKBVKEVATLSCCHNVSVBELAQTRIHWQKBKKAVVLTVMSGD mgy trrogispskcpylkrprollvlaglshlcsgvihytnbvkævatlscohnvsgeblagtriywokbkkomlitmwygd MGHTRRQGISPSKCPYLKPFQLIVIACISHFCSGVIHVTKBVKEVATISCGHNVSVEELAQTRIYAQKBKKAVIJTAMSGD mshtrrqi spskʻpylmppqlivlaslshpcsgv i kvtxbvatlscglinvsvbelaqta i ynqxekknvlitmasgd mohtrrogisppkcpylayfqollvlacishfcsgvihvtxbvkevatiscohnvsvbelaotrihnokexkavlthansod mshtrrogispskcpylkffqllvylacishfcsgvihvtkevkevatlscomnvsveelaqtrihmokekkmvltmmsd mshtrrqaispskopylkppqllvtaslshfosgvihvtkevktrvatlscomnusvbelaqtrihmqkekomvldmmsdd MGHTRRQGTSPSKCPYLKFPQLLVLACLSHPCSGV1HVTXBVKEVATLSCGMNVSVBELAQTR1HMQKEKXMVJJMMSGD MGYTRRQGTSPSKCPYLKFFQLLVLACLSHFCSGVIHVTRBVKEVATLSCCMNVSVEELAQTRIHWQKEKKKNVLTMMSGD mshtrrogtspskcpylkffqllavlaslshfcsgvihvtxbvkbyatlscglinvsvbelaqtri ynqkekkmvltmmsgd msktrrogispskopyinffrlivlaslshfosgvihvtkevkevatlscomnvsvrelaqtrihmokekkavvlymagd mshtrrogdispskcpylkfpqllvtaslshfcsgvinmtkgvkevatlscgrnvgvbellaqtriymqked mgytrrogispskcpylkffqllvvlacishfcsgvihvtxbvkbyatiscoanvsvbelaqtriymqkedtamasod mshterqoi spskcpylkpfqllvlaclshfcsovi hvtxbvkbyatlacchnvsvbblaqtei ymokbknyvltmmscd mgntrrqgispskcpylaffqllvlaglshfcsgvihvtkevkkvatlscchnvsveelaqtriyngkgkonvlymmscd mohterogi spskcpylkf pollvylacilshicsgv ihvtkevkevatlscolnvsveelaotet imokekknavlimmsod

SEQ:278_Human_B7-1

3 Ξ 3 3 Ξ 3 Ξ Ξ 3 Ξ 3 Ξ Ξ 3 $\Xi\Xi$ SEQ:085_R2_CTLA48P-5x4-11d SEQ:086_R2_CTLA48P-5x4-12c SEQ:087_R2_CTLA48P-5x4-1f SEQ:088_R2_CTLA48P-5x5-2e SEQ:089_R2_CTLA48P-5x5-2e SEQ:074_R2_CTLAMBP-5x2-10c SEQ:075_R2_CTLAMBP-5x2-11d SEQ:076_R2_CTLAMBP-5X2-12F SEQ: 077_R2_CTLA4BP-5x2-29 SEQ: 078_R2_CTLA4BP-5x2-3c SEQ: 079_R2_CTLA4BP-5x2-4c SEQ:080_R2_CTLA4BP-5x2-7b SEQ:081_R2_CTLA4BP-5x2-8c SEQ:082_R2_CTLA4BP-5x3-10e SEQ:083_R2_CTLA4BP-5x3-11b 8EQ:069_R1_CTLA4BP-5 SEQ:070_R1_CTLA4BP-7 SEQ: 072_R1_CTLA4BP-13 SEQ: 073_R1_CTLA4BP-27 88Q:084_R2_CTLA4BP-5x3-6F SEQ:090_R2_CTLA4BP-5x6-9d SEQ:091_R2_CTLA4BP-5x8-1f SRQ:092_R2_CTLA4BP-5x9-12c SE0:222_ctla5x9d10 SEQ: 071_R1_CTLA4BP-11

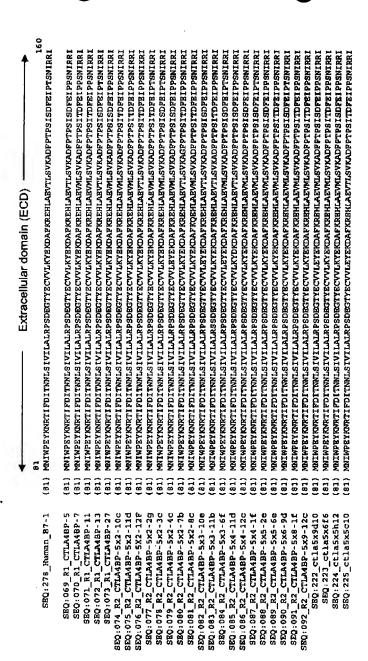
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Fig. 3A

MGHTRRQGTSPSKCPYLKFPQLLVLAGLSHLCSGVIHVTXBVKEVATLSCGHNVSVBELAGTRIYWQKEKKNVLTMAGGD MSHIRRQGISPSKCPYLNFPQLLVLACLSHFCSGVIHVTKBVKEVATLSCGHNVSVBELAQTRIYMQKEKKMVLTFMSQD MSHTRRQGTSPSKCPYLKFPQLLV1ASLSHPCSGV1HMTKBVKEVATLSCGPNVSVRELAOTR1YWQKEKRAVLTYMSGD MSHTRRQG1SSSKCPYLKFFQLLVLACLSHFCSGV1HVTKKVKBYATLSCGHNVSV2ELAQTR1YWKKHKNVLTPMSGD MGYTRRQGTSPSECPYLKFFQLLVLAGLSHPCSGVIHMTK&VKGVATLSCQLAVSVBELAQTRIHNQKEKNAVLTMASGD mshtrrqdi spskcpylnffrllvlaslshfcsqv i hvtkevktvatlscchnvgveelaqtr i hnokekknvl tymggd MSHTRRQGISPSKCPYLKFPQLLVLASLSHPCSGVIHVTKBVKBVATLSCGHNVSVBELAQTRIYWQKEKYMVL1MMSGD MGHTRRQGI8PSKCPYLKFFQLLVLASLSHFCSGVIHVTKEVKEVATISCGLAVSVBELAQTR1YMOKEKKMYLTMMSGD MGYTRRQGT8PSKCPYLNFRQLLVTASLSHFCGGVIHVTXEVKEVATLSCGHNVPVBELAQTR1YWQKEKHGVVLTRASGD MGHTRRQG19P8KCPYLKFPQLLVLACLSHFCSGV1HVTKBVRGVATLSCGHNVSVBELAQTR1YWQXDKHNVLJT9MSGD MGHTTRRQGTSPSKCPYLKFPQLLVLAGLSHPCSGVIHVTKBVKBVATLSCGHNVSVBBLAQTRIHNQKEKKNVLTROSGD MGHTRRQG18PSKCPYLKPPQLLVLACLSHPCSGV1YVTKBVKBVATLSCGHNVSVBELAQTR1YNQKEKKMVL1MMSQD mohttrrogtspskcpylkffrollylaglghpcsgylhytkbykgyatlscghnysybblaqtrindkekknylltrisg MGYTRRQGTSP8KCPYLNFPQLLVLASLSHFCSGVIHVTKBVKBVATLSCGHNVSVZELAQTR1HWQKEKRMVLTMMSGD MGYTRRQGISPSKCPYLKFFQLLVLAGLSHFCSGVIHVTKBVXBVATLSCGHNVSVEBLAQTRIHWQKEKMYVLTVMSGD MSHTIRRQGI SPSKCPYLKFFQLLVLAGLSHFCSGV I HVTKBVKGVATLSCQHNVSAERLAQTR I YMQKEKNOVLTIMISGD MGHTRRQG18PSKCPYLKFFQLLVLAGLSHPCSGVIHVTK8VKBVATLSOGLAVSV5BLAQTR1HWQKEKIOMVLTMMSGD MGYTRRQGISPSKCPYLKFFQLLVLACLSHFCSGVIHVTKRVKBVATLSCGHNVSDEELAQTRIHWQKEKKMVLTYMSGD MGYTRRQGISPSKCPYLKFFQLLVIAGLSHLCSGV1HVTKBVKBVATLPCGHNVBVBELAQTR1HNQKBKNOVLTMMSGD MGHTRRQGI SPSKCPYLKFPQLLVTAGLSHLCSGV IHMTKGVKEVATLSCGHNVSVEELAQTR I YRQKEKMVLTMMSGD KGHTRRQG1SPSKCPYLKPFQLLGLACLSHPCSQV1HVTXBVXBVATLSCGHNVSVBBLACTR1HNQKEKHYVLTRASGD mshtirrogispskopylkfyolivlacishpcsgvihvtkevkbvatisconnvsvblaogtrihnokekromvlitmmsgd NGHTRRQGTSPSKCPYLKFFQLLVLAGLSHPCBGV IHVTXBVXEVATLSCGHNVSVEBLAQTRI YYQKEKKNYLTMMSGD KSHTRRQG1SPSKCPYLKPPQLLVLASLSHFCSGV1HVTKBVKGVATLSCGHNVBVEELAQTR1YNQKEKRAVLTHMPQD mshttrqgispskcpylkppqllvlaqlshpcsgvihvtxbvkgvatlscghnvsveblagtrihwqkekgayvltpmsgg MGYTRRQOTSPSKCPYLKPFQLLVLACLSHFCSGV I HVTYGVKGVATLSCGHNVSVEBLAOTR I YRQKEKMYVLTMMSGD MGHTRRQCTSPSKCPYLNPFQLLVLACLSHPCSGVIHVTXGVKBVATLSCGHN/SVEBLAQTR1YRQKEKMYL,TMMSGD MGHTRRQGISPSKCPYLKFFOLLVLACLSHFCSGVIHVTKBVKEVATLSCGHNVSVEBLAQTRIHNOKEKGGVVLTMMSGD Extracellular domain (ECD) Signal sequence 3 ਰ Ξ Ξ 3 3 Ξ 7 7 Ξ 3 3 88Q:246_ctla2x2fl 58Q:247_ctla5x4hl 58Q:248_ctla5x4al SEQ:249_ctla5x2fl SEQ: 233_ctla5x1f1 SEQ: 234_ctla5x1d7 SEQ:236_ctla2x4a6 SEQ:237_ctla2x2f3 SBQ:235_ctla2x4g9 SEQ: 240 ctla2x1f10 SEQ: 252 ctla2x3h2 SEQ: 286_CTLA4BP_CON SEO:226_ctla5x3e8 SEQ:227_ctla5x3c4 SEQ:228_ctla5x3c3 SEQ: 229_ctla5x2h11 SEQ:230_ctla5x2d7 SEQ:231 ctla5x2b7 SEQ: 232 ctla5x2b1 ns SRQ: 238 ctla2x2f12 SEQ:239 ctlazxlg8 SEQ:241 ctla2x1c9 SEQ:242 ctla2x1h12 SEQ: 243_ctla2xle2 SEQ: 244 ctla2x1c4 SEO:245 ctla2x1b12 3EQ:250_ctla5x2e12 SBQ:251_ctla2x4h11

Fig. 3B



MNI WPEYKURTI FDI TNNLS IVI LALRPSD BGTYECVVLEYEKDAFKRBHLAEVTLSVKADFPTPSISDFEIPTSNIRRI mninpeyknrtifditnnisivilalrpsdrgtyecvvlkybkdapkrehlaevtlsvkadfptpsisdfeippsnirri MNI WPECKORTI FDI TWNLSI VI LALRPSDRGTYSCAVLKY EKDAFKREHLA EVTLASVKADFPTPSI SDFEI PISNIRRI MKI WPEYKORTI FOI TWILLSI VILALRP BOBGTYBCVVLKY EKOAFWEHLA EVMLSV KADFPTP BI BDFBI PPSNIRKI mnimpeyknrtifditnnlsivilalrpsdrgtybcvvlkybkdapkrehlabytlsvkadfptpsitdfeippsnirri MNI WPEHKMRTI FDI TWNLSI VI LALRPSDBGTYBCVVLKYEKDAPKRBHLARVMLSVKADFPTP91 SDFBI PPSNIRRI mniwpehkartifditmnlsivilalrpgdbgttgcvvlkyekdarkrehlaevtlgvkadfptesitdfpfbipgsnirri mai wpeymrti foi tanlsi vi **lale**pedrgtygcyvleyekdafkrehlaeymlsykadfptpsitdlei ppsnirri MNIWPEYKNOTIFOITNNISIVILALRPSDEGTYECVVLKYEKDAFKOEHLAEVMLSVKADFPTPSISDFEIPPSNIRRI mni wpeykmrti pditunlsivilalrpsdegtybcvvlkybkdafkrehlarwlsykadfptpgisdfpsnirri mnimpeykmrtifoitnnlsivilalrpsdegt-ecvvlkyekdafkrehlarvtlsvkadfpppsgippsnirri mniwpeymmtifditmnisivilalrpsdegtygcvvleyekgaftrbhilabymlsvkadffpgisdfeippsnirri mai wpeykarti foi tanlsavu i lalrpsdegtybcuvlkyekdafkarhlakytlsukadfptpsi i ppsnirri mninpeykartifditanlsivilalrpsdegtyrcvvlkyekdafyrhlafvalsvkadfptpsitdfippsnirri MNIWPEYKNRTIFDITMNLSIVILALRPSDEGTYBCVVLEYEKDAFKRBHLAEVMLGVKADFPTPSITDFEIPTGNIRRI MNIGPEYKNRTIFDITMNLSIVILALRPSDEGTYBGVVLKYEKDAFKRBHLABVMLSVKADFPTPSITDFEIPPSNIRRI mnindeykartifditanlsivilalrpsdegtybcvvlkyekdafyrehlabytlsvkadfptpsisdfeippsnirri mniwpeykartifditanlsivilalwesdegtybcvvlkybkodafyrrhilabynlsvkadffpeitdfeippenirri milypeyknrtifditnnlsivilalrpsdegtyrcvalkybkdafkqbhlaeytlsvkadfptsgisdfeippenirri MNI WPEYKNRTI FOITNNISI VII LALRISDEGTY BCVVLKY EKOAFKREHLA EVTIS VKADFPTPSISOFEI PTBNIRRI MNIKPEYKNRTIFDITNNISIVILAIRPSDEGTYBCVVLKYSKOAFKRKHLABVMLBVKADFPTPSISDFEIPTSNIRRI mminpehkartifditanlsivilalrpsdegtyecvvlkybkobfkrehllbykodffpsitdfeipfsnirri mniwpeykmrtifditunisivilalrpsdegtyrcvvlryekdafkrehlabytlsvkadfptpgibdfbipri maiwpeykartifditanlsivilalvilaerpsdegtybcovlkybrodafxrrhilabytlsvkadffptbsibdfelpfsviptfyiri MNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYBCVVLBYEKDAFKREHLABVMLSVKADFPTPSISDFEIPPSNIRRI mnimpeykartipditanisivilalrpsdegtyrcvolkyedarpakarhlarvalsvkadfptpsisdfeippsnirri MN IMPBYKNRTI I PD I TRNLLS I VI LALRPSDBGTY ECVVLKY BKDAFKREHLABVMLSVKADPPTPSI SDPSI PPSNIRK I MNIMPEYKORTIFDITNNLSIVILALRPSDBGTYBCVVLKYEKDAFKRBHLAEVTLSVKADFPTPSISDFEIPTSNIRRI Extracellular domain (ECD) 83 81) 81) 81) 81) 81) 81) 91 61) 81) 61 61) 61) 83 81) 81) 81) 81 83 61 81) 3 8 81) 83 SEQ:233_ctla5x1f1 SEQ:234_ctla5x1d7 SEQ:235_ctla2x4g9 SEQ:246_ctla2x2f1 SEQ:247_ctla5x4h1 SEQ:248_ctla5x4h1 SEQ:236_ctla2x4a6 SEQ:237_ctla2x2f3 SEQ:239 ctla2x1g8 SE0:241_ctla2x1c9 SEQ:242_ctla2x1h12 SEQ:243_ctla2x1e2 SEQ:244_ctla2x1c4 3EQ:250_ctla5x2e12 ctla2x4h11 3EQ:286_CTLA4BP_Con SE0:226_ctla5x3e8 SE0:227_ctla5x3c4 SEQ:228_ctla5x3c3 SEQ: 229 ctla5x2h11 SEQ:230_ctla5x2d7 SEQ:231 ctla5x2b7 SBQ:232 ctla5x2bl ns SEQ:238 ccla2x2f12 SEQ: 240 ctla2x1f10 SBO: 245 ctla2x1b12 SEQ:249_ctla5x2f3 9EQ:252_ccla2x3h2 SE0:251

Fig. 3D

		Extracellular domain (ECD)
		161
SEQ:278_Human_B7-1	(161)	(161) ICSTSOGFPEPHLSWLENGEELNAINTTVSQDPFTELYAVSSKLDFNMTTNHSFMCLIKYGHLRVNGTFNMTTTXQEHFF
SEQ:069_R1_CTLA4BP-5	(191)	ICSTSGGPPEPHLSRLENGESLNAINTTUSODPGTELVTVSSR1.DBN#TTNB19 DMC1.1 EVOLUT D1BNCTDNAMEN DC
SEQ: 070_R1_CTLA4BP-7	(161)	ICLTSGGFFBBRLAWMCGGELNAISTTVSGDFGTEL/AVSSKILDENTTRIJETRATITETTUR VOLLI BUNDET SAGBARF
SEQ: 071_R1_CTLA4BP-11	(161)	ICSTSGGFPEPHLPWLENGEELNAINTTVSGDFFTELFAVESKLIDENMTTPHSFMT1.1 FYGHI STROOTENAMTHER
SEQ: 072 R1 CTLA4BP-13	(161)	ICSTSGGFPEPHLFGLENGEEINAINTTASGOPETELTTVSSG.DPNMTPNRSSVG.1FVGHTIDNAFFRANKAFFRANKAFF
SEQ: 073_R1_CTLA4BP-27	(161)	I CSTSGGFPBPHLSWLENGBELNA INTTVSGDPBTELTTVSSKI DENMTANHSGTOLI EVOUH DYNAMERIEFE
SEQ:074_R2_CTLA4BP.5x2-10c	(161)	I CSTSGGFPBFHLSWLENGBELAN I NTTVSGDFFTBL VTVSSKILDFNWTANTSFYCT. I VYGH 1. 919-DF FNAULT F
3EQ:075_R2_CTLA4BP-5x2-11d	(161)	ICSTSGSF2EPFLFWLENGEELNAINTTVSGDPETELYTVSSKQ.DFNWTTPRSSYCT.TXVGHI.EVINATERMEATER
SE0:076_R2_CTLA4BP-5X2-12F	(161)	I CSTSGGFPBPHLSWLBNGEELNAINTTVSQDPBTELYTVSSKLDFWHTTNHSFWCL.1KYCHI DVNATTBWANTEVARTER
SEQ: 077_R2_CTLA4BP-5x2-2g	(161)	ICSTSQFPEPHLSWLENGERIANAINTTVSQDPETELYTVSBKTLDFWTTVHSSPMCLIKYCHIAVNOTTANAVTERVALTE
SEQ:078_R2_CTLA4BP-5x2-3c	(161)	ICSTSOGFPEPHLSWLENGERLWAINTIVSODPETGLYTVSSKLOFWHTTWNSPMCT.TXYCHTAVNOTENWAFER
SEQ:079_R2_CTLA4BP-5x2-4c	(181)	ICSTSOGFPEPHLSWLENGEBINGINTTVSQDPETELXTVSSXQDFNTTNRSFVCLITXXXXITANNAMPHXOPUPD
SEO:080_R2_CTLA4BP-5x2-7b	(191)	ICSTSQGPFEPHLSWLENGERIAAINTTV8ODPGTELYTVSSKT.DPNWTANH9FVCT.1 KYGHT BIRLYDDENGERF
SEQ:081_R2_CTLA4BP-5x2-8c	(161)	ICSTSGGPEPHLFWLENGEELNAINTIVSGOPETEL/AVSSKILDFWTTTMHSEVCT1 KVTHI DYNATTENAMEN PORTER
SEQ:082_R2_CTLA4BP-5x3-10e	(161)	ICSTSGGPPBPHLFWLENGEELMAINTTVSQDPETELYAVSSKLDFWTTTNHSFMCTFFWMTTPWOFULT
SEQ:083_R2_CTLA4BP-5x3-11b	(161)	ICSTSGGPPRPHLSHLENGEELMAISTTVSGOPETEL/TVSSKLDFWTTVNRGF/FFT I KYTHTI DVM/Y-FFMANTAR-FFF
SEQ:084_R2_CTLA4BP-5x3-6f	(161)	ICSTSGGPBPHLSWLENGEELNAINTTAAGODFEELYTVSSKLDFWTTVHRPWGT, FYTHTI PUNTTENENENENENENENENENENENENENENENENENEN
SED:085_R2_CTLA4BP-5x4-11d	(191)	ICSTSGGFFBPHLSHLSHLSHLSHLTVSGDPBFBLTTVSSKLDFWFTANHSFVCT. I VYGHT DYMAYDDAWAYDAWAYDAWAYDDAWAYDAWAYDDAWAYDAWAYDDAWAYDAWAYDAWAYDAWAYDAWAYDAWAYDDAWAYDA
SEQ:086_R2_CTLA4BP-5x4-12c	(191)	ICSTSGGFPEPHLPWLENGEELNAINTTVSQDPRTELYTVSSKLDFNKTTNHSSPMCI.JKYCHIAVANTFDRAFF
SEQ:087_R2_CTLA4BP-5x4-1f	(161)	ICST8GGFP8PHLFWLRNGEBLWAINTTVSQDBFT8LYTVSSXLDFWHTTWBSFWCL.FKYGHIRVWHTPWRWFPRABUPD
8EQ:088_R2_CTLA48P-5x5-2e	(161)	I CST8GGFPBPHLSWLBNGBBLNAINTTVSQDPBTBLYAVSSKLDFWTTNHSFWCLIKYCHLRVNOTTBNBFTDROBUED
SEQ:089_R2_CTLA4BP-5x5-6e	(161)	I CSTSGGFPEPHLS#LENGEBLNA.ISTTVSQDPETELYTVS\$KLDPNHTYTWHSPMC1.IXVGHLPNNOTT#NAMTT#NEHEB
SEQ:090_R2_CTLA4BP-5x6-9d	(191)	I CSTSGGFFFPHLSHLENGEBLNAINTTVSGDPFTELYTVSBKLOFNMTANHGFVCH I KYCHLENDIOTFFLLMTPKAEUE
SEQ:091_R2_CTLA4BP-5x8-1f	(161)	I CSASGGPPEPHI PWLENGEBLNAI NTTVSQDPETELYAVSBKLOPNMTTNN9 BWG1. IR YGHLRVNDTFFUNTPKARUED
SEQ: 092_R2_CTLA4BP-5x9-12c	(161)	I CSTSGGPPEPHLSWLENGERINAI NTTASQDPETELYTVSSKLDENMTTNYSFMCLI KYGHLRUNOT FNUKTPPRARUP
SEQ: 222_ctla5x9d10	(191)	ICSTSGGPPEPHLSNLENGEBLNAINTTASQDPGTELYTVSSKLDPNMTTNNSFMCLIKYGHLRUNOTFWWTTPKGRUPP
SEQ:223_ctla5x6f6	(161)	ICSTSGGFPEPHL FWLENGEBLNAINTTVSQDPETELYTVSSKLDFNMTTNRSFVCLI KYGHLRVNOTFNMNTPROSHFP
SEQ: 224 Ctlasx5h12	(161)	I CST3GGPFEPHL8WLENGBBLNAINTTVSQDPGTEL/YTVSSKLDFNMTTDRSFVCLI KYGHLRVNOTFNMTTPRGEHFP
SBQ:225_ctla5x5c10	(161)	I CSTSGGFPEPHLFWLENGEELNAISTTVSQDPETELYAVBSYLDFWATTWHSFWCLI KYGHLRVNQFFWNTTKQBHPP

Fig. 3E

		Extracellular domain (ECD)
		161
SRQ:226_ctla5x3e8	(191)	ICSTSGGFPEPHLFWLRNGEBI.NAINTTYGODPETELYTYSSKLDPNMTANHSEVCI.1 KYGHI.BYNYTRNBKRTBKGDPUPD
SEQ:227_ctla5x3c4	(161)	ICSTSGGFPEPRLAWMEDGEELMAINTTASGDPETELYTVSSKLDFNWTTNRSFVCI.IKYGHIRVNOTTERMATTDRONZUPD
SEQ:228_ctla5x1c3	(191)	ICSTSGGFPEPHLSMLENGEELNAINTTVSQDPGTELYTVSSKLDPNYTTNHSFMCLIKYGFLFPUNGTERVENTTPKORTUPD
SBQ: 229_ctla5x2h11	(161)	ICSTSQGFPEPHLFWLBNGBELNAINTTASQDPBTELYAVSSKLDFNMTTWRSFMCLJKYGHJRVNNTPANWTPKDRUPD
SEQ:230_ctla5x2d7	(161)	ICSTSGGFPEPHLSWLSNGSELAAINTTVSQDPSTGLYTVSSKLDPWYTTMSSPYCLIKYGGHRVNGTPNARHED
SEQ:231_ctla5x2b7	(191)	ICSTSQGFPEPHLSWLSWLSWGEELMAINTTVSQDPGTELYTVSSYLDFWMTANBSBVTLITYTTANGTERWATTSWARTER
SEQ: 232_ctla5x2b1 ns	(161)	ICSTSGGFPEPHLSWLSNGSELNAINTTVSQDPSTELYTGSSKLDFNFTTHISPMCLITYTGHLPUNTESGAFOKKEUPD
SEQ:233_ccla5x1f1	(161)	ICSTSQGPPEPHLFWLBNGBELNA INTTASQDPETELYTVSSYLDFNWTANHSPVTI.J KYGHI RVNOTFEVORUPO
SEQ: 234_ctla5x1d7	(161)	ICSTSOGPPEPHLFWLRNGBELNAINTTASODPETELYAVSSKLDFWFTTNHSFMCT.TXYGRLRVNOTFWNTTPXONHTP
SEQ:235_ccla2x4g9	(161)	ICSTSQGPPEPRIAMMEDGEELNAISTTVSQDPGTELCTVS8KLDFWRTTNH8PMCI.IRYGTI.RYGTARANTERNOFER
SBQ: 236_ctla2x4a6	(161)	ICSTSGGPPEPHIFWLEWLENGEELNAISTTVSQDPETELYAXSSGLDFWTTNHSPMCI.IXYGHIRVMOTERMANTERONEE
SEQ: 237_ctla2x2f3	(160)	ICSTSGGFPEPHLS#LENGEELIN INTTVSQDPGTELYTVSSKILDFWRTTNHSFWCT, IXYGRT, RUNGTFRWNTFDX/DENED
SEQ:238_ctla2x2f12.	(161)	ICSTSGGPPBPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFNYTTNRSFMCI.IKYGHIRANOTFRANTENOPHED
SEQ: 239_ctla2x198	(161)	ICSTSQGFPEPHISHLENGEELNAINTTV9QDPGTELTTV8SKIDFNFTTRRSFVCLIKYGHIRVNGTFRNAFFRANGE
SEQ:240_ctla2x1f10	(161)	ICSTSGGFPRPRIAMEDGEELNA INTTVSQDPGTELYAVSBKIDFNATYRHSPNCLIKVORI.RVNCTBNATTDROTHED
SEQ:241_ctla2x1c9	(161)	ICSTSGGFPBPRLAWMEDGEELNA I STTAGODPETELYTVSSKLDPWITTNHSFMCLI KYCHLRVMOTFMANTENCEMED
SE0:242_ctla2x1h12	(161)	ICSTSGGFPBPHLSWLENGEBLINAINTTV3QDPGTBLYTV3SKLDFWTTNH9FWCLIKYGHLRVNOFFRWNTPKORHP
SEQ:243_ctla2x1e2	(161)	ICSTSGGFPEPHLSWLENGEELNAINTTVSQDPGTELYTVSSKLDFNMTTNHSFWCLIKYGHLEVNOTBNNTTPKORHFP
SEQ:244_ctla2x1c4	(161)	ICSTSGGFPBPHLFWLENGEBLNAINTTVSQDPGTBLYAVSSCLDFWFTNHURMCLIKYGHLRVNGFRANTFRORHFP
SEQ: 245_ctla2x1b12	(191)	ICSTSGGFPBPRLAMMEDGESTANITTVSGDFFTSLXTVSSKLDFWFTANNSFMCLIKYGHLRVNOFFNNTTPKORHPP
SEQ:246_ctla2x2f1	(161)	ICSTSGGFPEPHLFWLENGEELMAINTTASGDPETBLYTVSSKLDFWMTTNRSFWCLIKYGHIRUNGTFWWNTDROFFFE
SBQ:247_ccla5x4ht	(161)	ICSTSGGFPEPHLFWLENGEELNAINTTASGDPFTELYTYSSKLDFNYTTNRSFVCLIKYGHLRVNOTFRKNYTPKOFFTE
SEQ:248_ctla5x4al	(191)	ICSTSGGFPEPHLSWLENGBELNAINTTV9CDPGTBLYTVSSKLDPNATTNRSBVCLTFVGHTAUNGTFNANTDEGELT
SEQ:249_ctla5x2f3	(191)	ICSTSGGFPEPHLSWLENGEELNAINTTASQDPETELYTVSSKLDFNATTRRSPVCLIKKETTRUNGTFRUANTPKORMED
SEQ:250_ctla5x2e12	(161)	ICSTSOGFPEPHI.SWLRNGBELNAISTTVSQDPGTBLYAVSSKLDPNMTTNRBFVCLIKYGHLRVNOFFWNTTKNRHFP
SEQ:251_ctla2x4h11	(191)	ICSTSGGPPEPHISWLRNGBELNAINTTV8QDPGTELYAVBSXLDPNMTTNNSFMCL1XYGHLRVNOFFRWNTPKORHPP
	(161)	ICSTPGGFPEPRIAWMEDGREUNAISTTVSQDPGTEL/ANSSKLDFNMTTNHSFMCLIKYGHRUNDFRWNTTKORHFP
SEQ: 286_CTLA4BP_Con	(161)	I CSTSGGPPEPHLSWLENGEELNAINTTVSQDPITELYTVSSKLDFNWTTNHSFMCL I KYGHLRYNQTFNWNTPYQEHPP

Fig. 3F

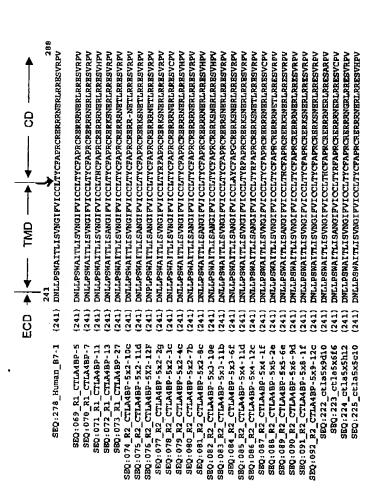


Fig. 3G

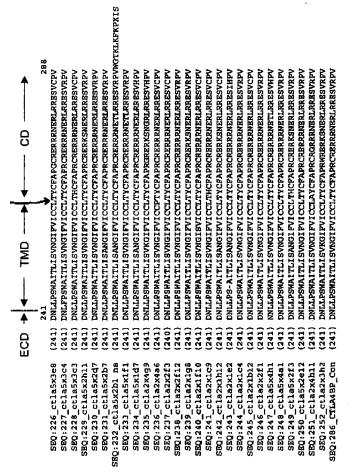
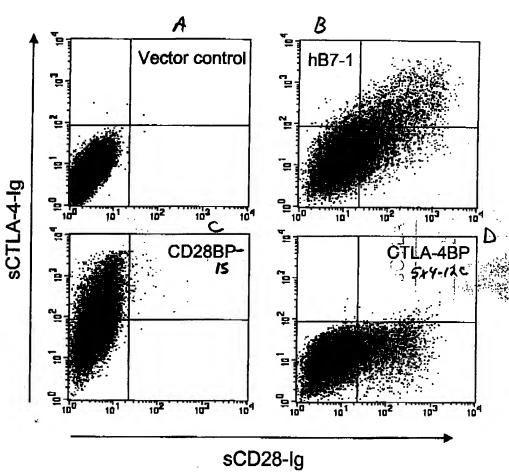


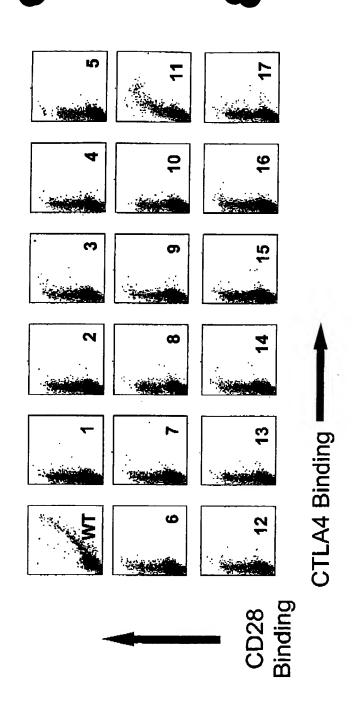
Fig. 3H

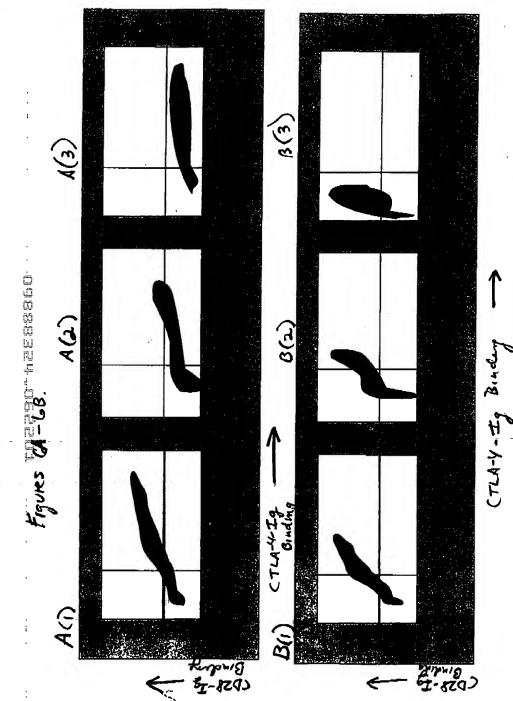


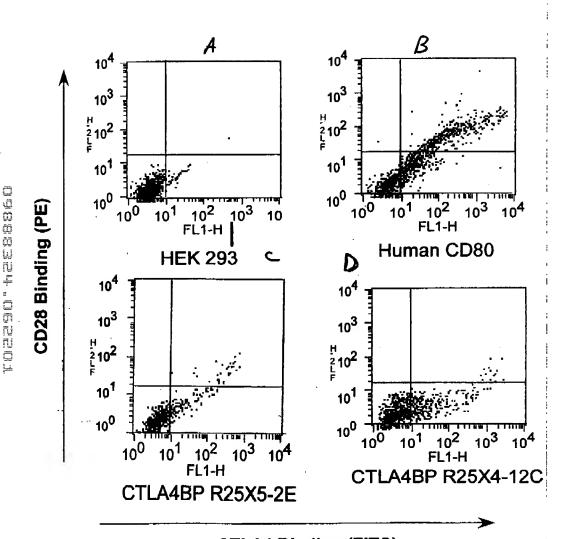
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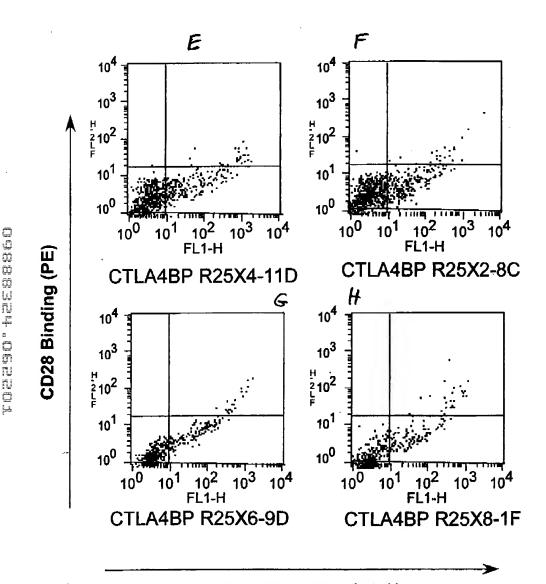
CD28BP after 2nd Round of Shuffling







CTLA4 Binding (FITC)



CTLA4 Binding (FITC)

TOPESO. TEFFERS & 4-8B

a CTLA-4BP - 5x4-12c

CD28BP-15

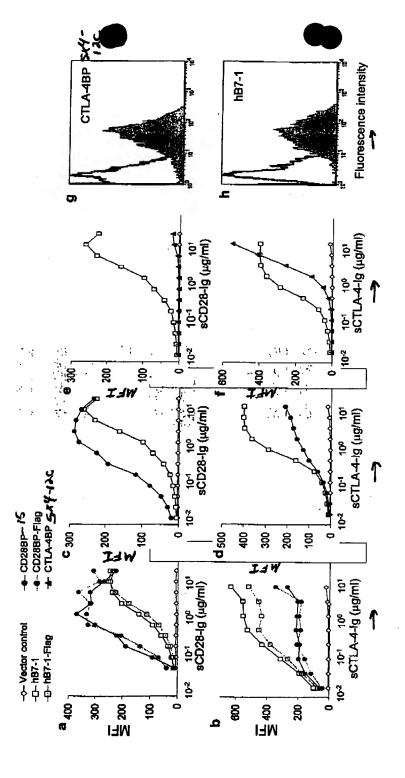
GAYKLEHLAŠVŘLŇÍŘADFPVPŤIŇDĽĞŇPŠĎNIRRĽICSTSGGFPŘPHLÝWLENGEELNAŤNT

COU - MINDAPIC COU

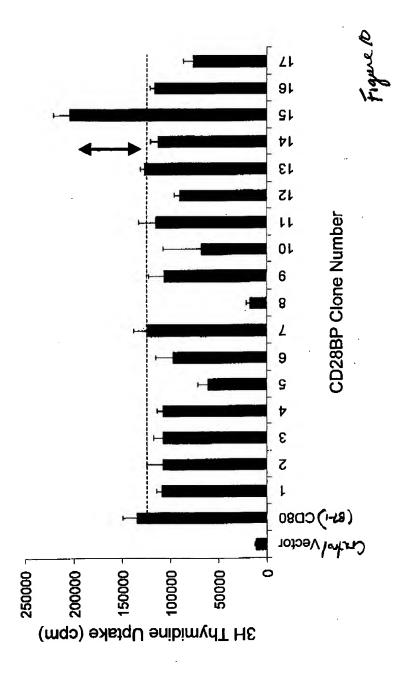
COU - MINDAPIC COU <u>**</u> <u>ŠĽRIYWQKĎŠKMVLĂĬĽPGKŶĞŶWPEYKNRTIŤDMŇĎNPŘIVILALRPSDŠGTYŤCVĬČKPŶĽK</u> TVSQDPĞTELYMİSSELDENYTÜNHSİVCLIKYGEL ŠVŠQİFPWŠKPKOEPPIDĞLPEMVIIPVŞ <u>MGHTŴŔŴGŜĹPPKŘPČLŴĽŠQLLVLŤGLĚŤFCSGĬŤPŘŠVTKŘVKEŤVŇLSCĎŤNŤSŤEELŤ</u> ĠĂĽVĽŤĂŶŶĹŶ¢ĹACRĤŶĂŘŴĸŘŤRRŇĚEŤŸĞŤEŘĽŠPĬŶĹĞŠĀĞŠŠĞ

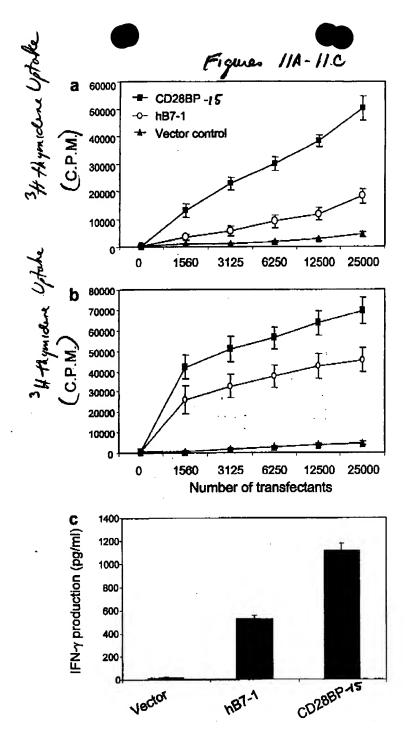
rhesus/baboon rabbit orangutan baboon human rhesus

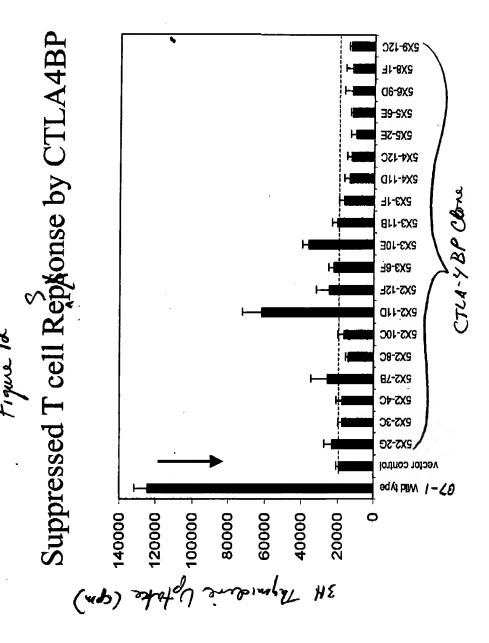
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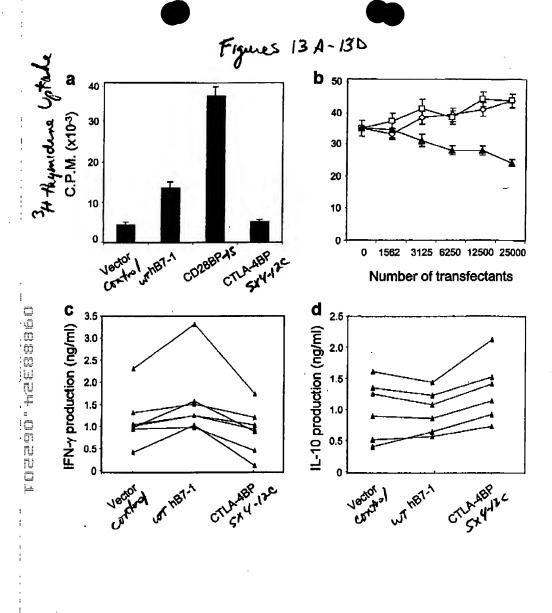


Figures 9A-9#









Soluble Forms

Human B7.1 sECD

AAAGAPVPYPDPLEPPR AAHHHHHH

VIH......TTKQEHFPDN

E-epitope His-tag

(35-242)

(1-34)

Extracellular Domain

Signal

(243-259) (260-268)

Human B7.1 ECD-lg Form ඛ

hinge -CH2-CH3 Bstell

Human IgG1 Fc Fragment PKSCDKTHTCPPCP...... GenBank Acc.# P01857 GVT VIH.....TKQEHFPDN B7.1 ECD (35-242)

14A - 14B

NCSM-sECD Expression Construct

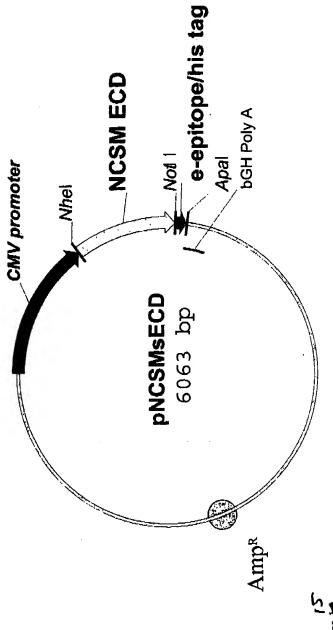


Figure 🝎

SDS-PAGE showing various soluble forms of wt & NCSM proteins

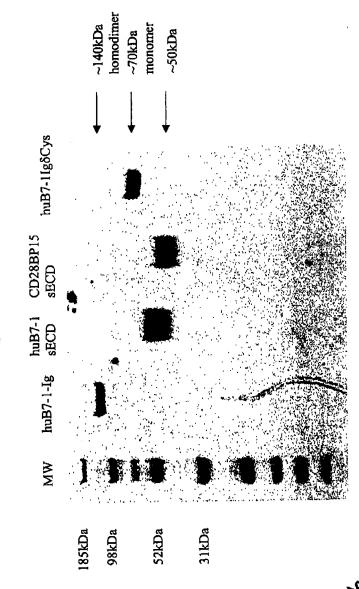
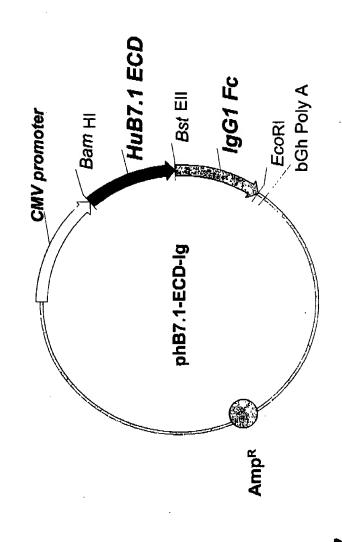


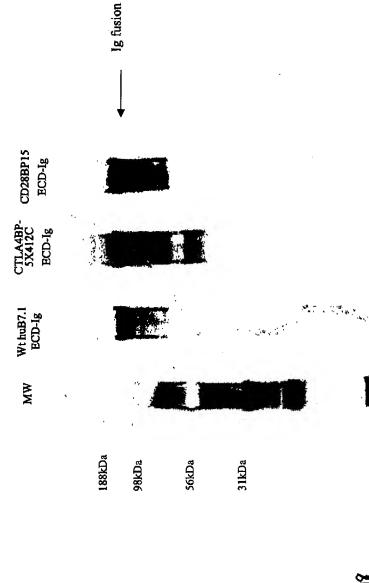
Figure *

B7-1-ECD-Ig Fusion Expression Construct



Figure

Scale-up Production of wild-type soluble Human B7.1-, CTLA4BP 5X4-12C-, and CD28BP-15 ECD-Ig Fusion Proteins





Expression of CTLA-4-BP-1g and CD28-BP-1g Proteins

54-1.78ud WW CTLA4-5X2-8C ECD-Fc CTLA4-5X4-11D ECD-Fc CTLA4-6X4-12C ECD-Fc CD58Bb-8 ECD-Lc CDS8Bb-11 ECD-Ec CD38Bb-12 ECD-Ec CTLA-45X5-2E ECD-Fc CTLA-5X6-9D ECD-Fc CTLA4-5X8-1F ECD-Fc

Vector



~140 kDa

~70 kDa

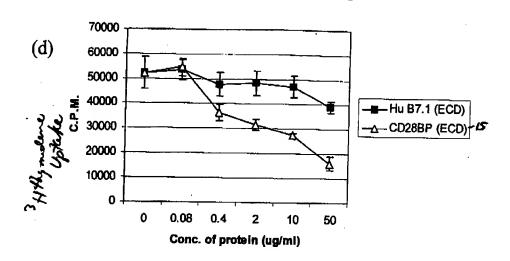
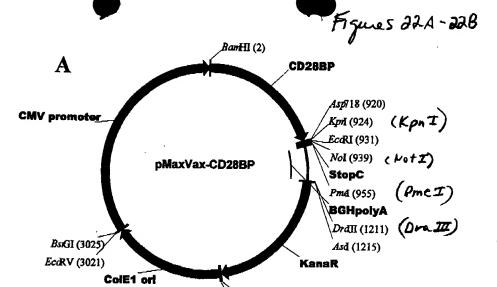


Figure 20D



NgdMI (2197)

Nhã (2203)

